GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 09:29:47 ; Search time 2881.61 Seconds
(without alignments)
130.718 Million cell updates/sec

Title: US-10-014-743-2
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	18	100.0	18	6	AR007529	AR007529 Sequence
3	18	100.0	18	6	AR012189	AR012189 Sequence
4	18	100.0	18	6	AR016075	AR016075 Sequence
5	18	100.0	18	6	AR022604	AR022604 Sequence
6	18	100.0	18	6	AR023877	AR023877 Sequence
7	18	100.0	18	6	AR024485	AR024485 Sequence
8	18	100.0	18	6	AR030639	AR030639 Sequence
9	18	100.0	18	6	AR030808	AR030808 Sequence
10	18	100.0	18	6	AR036904	AR036904 Sequence
11	18	100.0	18	6	AR038851	AR038851 Sequence
12	18	100.0	18	6	AR044721	AR044721 Sequence
13	18	100.0	18	6	AR052368	AR052368 Sequence
14	18	100.0	18	6	AR055166	AR055166 Sequence
15	18	100.0	18	6	AR059043	AR059043 Sequence
16	18	100.0	18	6	AR065059	AR065059 Sequence
17	18	100.0	18	6	AR068722	AR068722 Sequence
18	18	100.0	18	6	AR079674	AR079674 Sequence
19	18	100.0	18	6	AR080255	AR080255 Sequence
20	18	100.0	18	6	AR085312	AR085312 Sequence
21	18	100.0	18	6	AR086107	AR086107 Sequence
22	18	100.0	18	6	AR089515	AR089515 Sequence
23	18	100.0	18	6	AR092061	AR092061 Sequence
24	18	100.0	18	6	AR112196	AR112196 Sequence
25	18	100.0	18	6	AR112299	AR112299 Sequence
26	18	100.0	18	6	AR116140	AR116140 Sequence
27	18	100.0	18	6	AR122269	AR122269 Sequence
28	18	100.0	18	6	AR128087	AR128087 Sequence
29	18	100.0	18	6	AR131243	AR131243 Sequence
30	18	100.0	18	6	AR141143	AR141143 Sequence
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ALIGNMENTS

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A49774
LOCUS A49774 18 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 5 from Patent WO9609395.
ACCESSION A49774
VERSION A49774.1 GI:2303068
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Meyer,T.F., Pohlner,J., Beck,S.C., Jose,J., Woelk,U., Lorenzen,D.R. and Oetzelberger,K.B.
TITLE DRUG FOR THE PREVENTION AND TREATMENT OF AUTO-IMMUNE AND VIRAL DISEASES, AND DIAGNOSTIC AGENTS FOR DETECTING SAID DISEASES
JOURNAL Patent: WO 9609395-A 5 28-MAR-1996;
MAX PLANCK GESELLSCHAFT (DE)
COMMENT Other publication AU 3651595 960409.
FEATURES Location/Qualifiers
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LOCUS       AR007529                  18 bp    DNA     linear   PAT 04-DEC-1998
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ACCESSION   AR007529
VERSION     AR007529.1  GI:3967013
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cigan,A.M. and Albertsen,M.C.
  TITLE     Reversible nuclear genetic system for male sterility in transgenic
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  JOURNAL   Patent: US 5750868-A 2 12-MAY-1998;
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Db      1 TGTAAAACGACGGCCAGT 18


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DEFINITION  Sequence 2 from patent US 5763243.
ACCESSION   AR012189
VERSION     AR012189.1  GI:3970179
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cigan,A.M. and Albertsen,M.C.
  TITLE     Reversible nuclear genetic system for male sterility in transgenic
            plants
  JOURNAL   Patent: US 5763243-A 2 09-JUN-1998;
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DEFINITION  Sequence 3 from patent US 5776680.
ACCESSION   AR016075
VERSION     AR016075.1  GI:3972352
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Leibowitz,M.J. and Liu,Y.
  TITLE     Diagnostic probes for pneumocystis carini
  JOURNAL   Patent: US 5776680-A 3 07-JUL-1998;
FEATURES             Location/Qualifiers
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DEFINITION  Sequence 2 from patent US 5792853.
ACCESSION   AR022604
VERSION     AR022604.1  GI:3976666
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cigan,A.M. and Albertsen,M.C.
  TITLE     Reversible nuclear genetic system for male sterility in transgenic
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  JOURNAL   Patent: US 5792853-A 2 11-AUG-1998;
FEATURES             Location/Qualifiers
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DEFINITION  Sequence 2 from patent US 5795753.
ACCESSION   AR023877
VERSION     AR023877.1  GI:3977171
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
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  AUTHORS   Cigan,A.M. and Albertsen,M.C.
  TITLE     Reversible nuclear genetic system for male sterility in transgenic
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  JOURNAL   Patent: US 5795753-A 2 18-AUG-1998;
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DEFINITION  Sequence 26 from patent US 5795976.
ACCESSION   AR024485
VERSION     AR024485.1  GI:3977779
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Oefner,P.Josef. and Underhill,P.Anton.
  TITLE     Detection of nucleic acid heteroduplex molecules by denaturing
            high-performance liquid chromatography and methods for comparative
            sequencing
  JOURNAL   Patent: US 5795976-A 26 18-AUG-1998;
FEATURES             Location/Qualifiers
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DEFINITION  Sequence 1 from patent US 5861287.
ACCESSION   AR030639
VERSION     AR030639.1  GI:5943853
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Metzker,M.L. and Gibbs,R.A.
  TITLE     Alternative dye-labeled primers for automated DNA sequencing
  JOURNAL   Patent: US 5861287-A 1 19-JAN-1999;
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DEFINITION  Sequence 11 from patent US 5861378.
ACCESSION   AR030808
VERSION     AR030808.1  GI:5944022
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Iwanaga,S., Kawabata,S.-i. and Saito,T.
  TITLE     Horseshoe crab hemocyte polypeptides, and preparation and DNA
            encoding thereof
  JOURNAL   Patent: US 5861378-A 11 19-JAN-1999;
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VERSION     AR036904.1  GI:5954760
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SOURCE      Unknown.
  ORGANISM  Unknown.
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REFERENCE   1  (bases 1 to 18)
  AUTHORS   Lee,L.G., Spurgeon,S.L. and Rosenblum,B.
  TITLE     Energy transfer dyes with enchanced fluorescence
  JOURNAL   Patent: US 5800996-A 2 01-SEP-1998;
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LOCUS       AR038851                  18 bp    DNA     linear   PAT 29-SEP-1999
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ACCESSION   AR038851
VERSION     AR038851.1  GI:5958214
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SOURCE      Unknown.
  ORGANISM  Unknown.
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REFERENCE   1  (bases 1 to 18)
  AUTHORS   Mukerji,P., Thurmond,J.Marie., Hansson,L., Baxter,J.Harris. and
            Hards,R.George.
  TITLE     Method for expressing phosphorylated recombinant human
            .beta.-casein in a bacterial system
  JOURNAL   Patent: US 5807702-A 3 15-SEP-1998;
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LOCUS       AR044721                 18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 40 from patent US 5817515.
ACCESSION   AR044721
VERSION     AR044721.1  GI:5966186
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Gallatin,W.Michael. and Van der Vieren,M.
  TITLE     Human B2 integrin alpha subunit antibodies
  JOURNAL   Patent: US 5817515-A 40 06-OCT-1998;
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ACCESSION   AR052368
VERSION     AR052368.1  GI:5975732
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Gallatin,W.Michael. and Van der Vieren,M.
  TITLE     Human .beta.2 integrin .alpha. subunit
  JOURNAL   Patent: US 5831029-A 40 03-NOV-1998;
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DEFINITION  Sequence 40 from patent US 5837478.
ACCESSION   AR055166
VERSION     AR055166.1  GI:5980743
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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REFERENCE   1  (bases 1 to 18)
  AUTHORS   Gallatin,W.Michael. and Van der Vieren,M.
  TITLE     Method of identifying modulators of binding between and VCAM-1
  JOURNAL   Patent: US 5837478-A 40 17-NOV-1998;
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DEFINITION  Sequence 2 from patent US 5837851.
ACCESSION   AR059043
VERSION     AR059043.1  GI:5984620
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cigan,A.M. and Albertsen,M.C.
  TITLE     DNA promoter 5126 and constructs useful in a reversible nuclear
            genetic system for male sterility in transgenic plants
  JOURNAL   Patent: US 5837851-A 2 17-NOV-1998;
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Job time: 6596 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 09:37:26 ; Search time 365.16 Seconds
(without alignments)
84.633 Million cell updates/sec

Title: US-10-014-743-2
Perfect score: 18
Sequence: 1 TGTAAAACGACGGCCAGT 18

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	18	100.0	18	17	AAT35004	Primer for amplify
7	18	100.0	18	17	AAT27188	Defensin coding se
8	18	100.0	18	18	AAT86529	5'-Terminal amine
9	18	100.0	18	18	AAV06702	Tagged M13 sequenc
10	18	100.0	18	18	AAV06703	5'-Terminal amine
11	18	100.0	18	18	AAV12872	Primer M13-21 for
12	18	100.0	18	18	AAV04321	Primer used in pre
13	18	100.0	18	18	AAT89488	Human recombinant
14	18	100.0	18	18	AAT89489	Human recombinant
15	18	100.0	18	18	AAT88395	Energy transfer fl
16	18	100.0	18	18	AAT85962	Human neuroblastom
17	18	100.0	18	18	AAT85969	Human K+ channel g
18	18	100.0	18	18	AAT85955	Human AMY gene det
19	18	100.0	18	18	AAT85976	Human NB Phox dete
20	18	100.0	18	18	AAT85983	Human neuro-D gene
21	18	100.0	18	18	AAT59186	FET-3 primer for f
22	18	100.0	18	18	AAT66206	Hepatitis C virus
23	18	100.0	18	19	AAV63816	Mouse alpha-d PCR
24	18	100.0	18	19	AAV62338	Human CS198 DNA pr
25	18	100.0	18	19	AAV41951	Nucleotide sequenc
26	18	100.0	18	19	AAV54625	LU105 EST-specific
27	18	100.0	18	19	AAV39468	Primer 21M13, used
28	18	100.0	18	19	AAV35262	Mouse beta-integri
29	18	100.0	18	19	AAV35328	DNA analysis metho
30	18	100.0	18	19	AAV26661	Human PS112 gene p
31	18	100.0	18	19	AAV36183	Oligonucleotide us
32	18	100.0	18	19	AAV23703	Primer based on F1
33	18	100.0	18	19	AAV17914	Mammaglobin univer
34	18	100.0	18	19	AAV15502	Forward primer for
35	18	100.0	18	19	AAV10884	Human MLH1 gene PC
36	18	100.0	18	19	AAV19689	Insecticidal toxin
37	18	100.0	18	19	AAV15297	Murine AGP-1 PCR p
38	18	100.0	18	20	AAZ09715	Bacteriophage M13
39	18	100.0	18	20	AAZ09404	HCV-1b ISD core re
40	18	100.0	18	20	AAX99693	M13-21 primer used
41	18	100.0	18	20	AAX80639	Oligonucleotide, P
42	18	100.0	18	20	AAX78713	Human pancreatic P
43	18	100.0	18	20	AAV72371	Human BS274 protei
44	18	100.0	18	20	AAX57992	PCR primer for Hum
45	18	100.0	18	20	AAX56224	Human alpha-7 nico

ALIGNMENTS

RESULT 1
AAQ39606
ID AAQ39606 standard; DNA; 18 BP.
XX
AC AAQ39606;
XX
DT 07-OCT-1993 (first entry)
XX
DE Fluorescence detection primer KM1.
XX
KW Polymerase chain reaction; PCR; amplify; primer; fluorescence;
KW detection; label; ss.
XX
OS Synthetic.
XX
PN JP05111399-A.
XX
PD 07-MAY-1993.
XX
PF 22-OCT-1991; 91JP-0274264.
XX
PR 22-OCT-1991; 91JP-0274264.
XX
PA (HITA) HITACHI LTD.
XX
DR WPI; 1993-184819/23.
XX
PT Fluorescence detection for nucleic acid sample - comprises
PT binding labelled oligo:nucleotide(s) to sample DNA, preparing
PT elongation chain by enzyme reaction, isolating different
PT fragments and detecting fluorescence
XX

PS Disclosure; Page 6; 7pp; Japanese.
XX
CC The sequences given in AAQ39604-09 are primers which were used in a
CC detection method to detect nucleic acid molecules. The primers are
CC fluorescently labelled. They are bound to a target nucleic acid
CC sample and elongated by PCR. The fluorescence of the amplified
CC sample is detected. This method can be used for the acurate
CC detection of nucleic acid sequences.
XX
SQ Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTAAAACGACGGCCAGT 18
||||||||||||||||||
Db 1 tgtaaaacgacggccagt 18

RESULT 2
AAT02863
ID AAT02863 standard; DNA; 18 BP.
XX
AC AAT02863;
XX
DT 14-MAR-1996 (first entry)
XX
DE Fungus-derived 18S rRNA encoding DNA sequencing primer.
XX
KW Polymerase chain reaction; primer; ribosomal RNA; amplification;
KW sequencing; Matsutake mushroom; ss.
XX
OS Agaricus bisporus.
XX
PN JP07177889-A.
XX
PD 18-JUL-1995.
XX
PF 22-DEC-1993; 93JP-0346106.
XX
PR 22-DEC-1993; 93JP-0346106.
XX
PA (RIKA) RIKAGAKU KENKYUSHO.
XX
DR WPI; 1995-279918/37.
XX
PT Oligo:nucleotide primer comprising amplification and sequencing
PT portions - useful for determination of fungal DNA sequences by PCR
PT amplification
XX
PS Claim 2; Page 2; 8pp; Japanese.
XX
CC AAT02855-T02860 are amplification primers for DNA coding for
CC fungus-derived 18S rRNA. These primers may be bound at the 5' end
CC to the 3' end of a sequencing primer (AAT02861-T02863). The
CC resulting oligonucleotide primers comprising amplification and
CC sequencing portions (AAT02864-T02869). These primers are useful for
CC the determination of the base sequences of fungi.
XX
SQ Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTAAAACGACGGCCAGT 18
||||||||||||||||||
Db 1 tgtaaaacgacggccagt 18

RESULT 3
AAQ90924
ID AAQ90924 standard; DNA; 18 BP.
XX
AC AAQ90924;
XX
DT 05-MAR-1996 (first entry)
XX
DE hMLH1 gene exon 16 second stage amplification primer N-19269.
XX
KW hMLH1; MutL homologue; cancer diagnosis; mismatch repair; tumour;
KW susceptibility; mutation detection; exon 16; primer N-19269;
KW second stage amplification; ss.
XX
OS Synthetic.
XX
PN WO9516793-A1.
XX
PD 22-JUN-1995.
XX
PF 16-DEC-1994; 94WO-US14746.
XX
PR 09-DEC-1994; 94US-0352902.
PR 17-DEC-1993; 93US-0168877.
PR 08-MAR-1994; 94US-0209521.
XX
PA (DAND) DANA FARBER CANCER INST INC.
PA (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI Baker SM, Bollag RJ, Bronner CE, Kolodner RD, Liskay RM;
XX
DR WPI; 1995-231583/30.
XX
PT Determn. of a mutation in a mutL homologue or gene prod. in a tissue
PT - used to diagnose cancer susceptibility, and to identify and
PT classify a DNA mismatch-repair-defective tumour
XX
PS Disclosure; Fig 4B-4; 168pp; English.
XX
CC AAQ90924 and AAQ90925 are a primer pair for the 2nd stage amplification
CC of the hMLH1 (a MutL homologue) gene exon 16. A mutation in an
CC analogous segment of a hMLH1 or hPMS1 nucleic acid isolated from a
CC subject, can be detected by comparing it with the above gene
CC fragment. This method can be used to diagnose cancer susceptibility,
CC or to identify and classify a DNA mismatch-repair defective tumour.
XX
SQ Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTAAAACGACGGCCAGT 18
||||||||||||||||||
Db 1 tgtaaaacgacggccagt 18

RESULT 4
AAQ91747
ID AAQ91747 standard; DNA; 18 BP.
XX
AC AAQ91747;
XX
DT 28-DEC-1995 (first entry)
XX
DE M13 primer.
XX
KW Beta-2 integrin alpha-d subunit; antiinflammatory; arteriosclerosis;
KW inflammatory bowel disease; asthma; polymerase chain reaction;
KW PCR; primer; ss.
XX
OS Synthetic.

XX
PN WO9517412-A1.
XX
PD 29-JUN-1995.
XX
PF 21-DEC-1994; 94WO-US14832.
XX
PR 05-AUG-1994; 94US-0286889.
PR 23-DEC-1993; 93US-0173497.
XX
PA (ICOS-) ICOS CORP.
XX
PI Gallatin WM, Van Der Vieren M;
XX
DR WPI; 1995-240603/31.
XX
PT Alpha sub-unit polypeptide of human beta 2 integrin - used to
PT identify potential antiinflammatory agents, for the treatment of
PT graft arteriosclerosis, inflammatory bowel disease, asthma, etc.
XX
PS Example 19; Page 58; 172pp; English.
XX
CC The probe based on human integrin alpha-d clone 19A2 (given in
CC AAQ91712) was used to isolate mouse alpha-d cDNA clones from a thymic
CC oligo dT-primed library in lambda ZAP II. Sequencing of isolated
CC clones was performed using M13 and M13 reverse.1 primers
CC (AAQ91747-48).
XX
SQ Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTAAAACGACGGCCAGT 18
||||||||||||||||||
Db 1 tgtaaaacgacggccagt 18

RESULT 5
AAT62669
ID AAT62669 standard; DNA; 18 BP.
XX
AC AAT62669;
XX
DT 21-MAY-1997 (first entry)
XX
DE Primer RO-4 for beta-casein cDNA amplification.
XX
KW primer; polymerase chain reaction; PCR; plasmid; modified protein;
KW expression; beta-casein; enzyme; kinase; inhibit attachment;
KW Haemophilus influenzae; prevent; treat; otitis media; children; ss.
XX
OS Synthetic.
XX
PN WO9627018-A1.
XX
PD 06-SEP-1996.
XX
PF 27-FEB-1996; 96WO-US02866.
XX
PR 06-NOV-1995; 95US-0554642.
PR 27-FEB-1995; 95US-0395239.
PR 06-NOV-1995; 95US-0554137.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Baxter JH, Hansson L, Hards RG, Mukerji P, Thurmond JM;
XX
DR WPI; 1996-412784/41.
XX
PT Plasmid to express modified recombinant proteins, esp. human
PT beta-casein in a bacterial system - encodes an exogenous protein
PT and enzyme which modifies the protein
XX
PS Example 5; Page 28; 58pp; English.
XX
CC To create a single construct designed for secretion of phosphorylated
CC protein to the periplasmic space of a bacterial cell, the beta-casein
CC encoding sequence is put into an expression vector containing a leader
CC sequence that directs protein transport toe the periplasm. PCR was
CC performed using the clone resulting from these procedures as the target
CC DNA and primers AAT62669-70. Novel plasmids of the invention comprise a
CC promoter, a sequence encoding an exogenous protein, especially human
CC beta-casein, and a sequence encoding an enzyme which can modify the
CC exogenous protein (e.g. a human kinase capable of phosphorylating
CC recombinant beta-casein in a bacterial system). The plasmids are useful
CC to produce a modified recombinant protein in a host cell, partic. human
CC caseins, cell receptor proteins, fatty acylated proteins, mammalian
CC muscle proteins, the gag polyproteins of retroviruses, or mammalian
CC proteins targeted by retroviral src kinases. The method can be used to
CC produce a recombinant human protein useful to inhibit attachment of
CC Haemophilus influenzae to human cells, which can prevent and treat
CC otitis media in children.
XX
SQ Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTAAAACGACGGCCAGT 18
||||||||||||||||||
Db 1 tgtaaaacgacggccagt 18

RESULT 6
AAT35004
ID AAT35004 standard; DNA; 18 BP.
XX
AC AAT35004;
XX
DT 28-NOV-1996 (first entry)
XX
DE Primer for amplifying 5126f anther specific promoter.
XX
KW Plant; sterile; sterility; male; reversible; anther; promoter;
KW pollen formation; ss.
XX
OS Synthetic.
XX
PN WO9617945-A1.
XX
PD 13-JUN-1996.
XX
PF 07-DEC-1995; 95WO-US15229.
XX
PR 07-JUN-1995; 95US-0474556.
PR 08-DEC-1994; 94US-0351899.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Albertson MC, Cignan AM;
XX
DR WPI; 1996-287189/29.
XX
PT Prodn of reversible male sterility in a plant - by transformation
PT with a construct with regulatory elements and DNA which inhibit
PT pollen formation of function
XX
PS Example 1; Page 33; 94pp; English.
XX
CC A construct comprising a DNA sequence encoding a gene product which
CC inhibits pollen formation or function, an operator controlling its

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CC   expression functionally linked to a promoter specific to cells
CC   critical to pollen formation can be used in the production of male
CC   sterile plants when inserted into plants and expressed.  When these
CC   male sterile plants are then crossed with pollen derived from a male
CC   fertility line, make sterile hybrid plants are produced.  These
CC   plants can then be made sterile or fertile depending on whether the
CC   incorported construct is expressed.  The method produces reversible
CC   male sterility in a plant. Two primers (AAT35004, AAT35005) were used
CC   to amplify a partial 5126 promoter cDNA clone which was used to
CC   identify a full length clone from a cDMA library.
XX
SQ   Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;


  Query Match             100.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.4;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGTAAAACGACGGCCAGT 18
          ||||||||||||||||||
Db      1 tgtaaaacgacggccagt 18


RESULT   7
AAT27188
ID   AAT27188 standard; DNA; 18 BP.
XX
AC   AAT27188;
XX
DT   20-NOV-1996  (first entry)
XX
DE   Defensin coding sequence primer #1.
XX
KW   Structural analogue; defensin; antibacterial; helmet crab;
KW   intrahemocyte fine granule fraction; gram positive; gram negative;
KW   fungi; germicide; preservative; wound healing; ss.
XX
OS   Synthetic.
XX
PN   JP08092286-A.
XX
PD   09-APR-1996.
XX
PF   01-SEP-1994;   94JP-0232025.
XX
PR   22-JUL-1994;   94JP-0191850.
XX
PA   (SEGK ) SEIKAGAKU KOGYO CO LTD.
XX
DR   WPI; 1996-236096/24.
XX
PT   Defensin structural analogue peptide(s) - useful as antimicrobial
PT   agents and germicides
XX
PS   Example 2; Page 14; 17pp; Japanese.
XX
CC   The sequences given in AAT27186-90 are a probe and primers which were
CC   used in the isolation of the full length defensin coding sequence.
CC   Defensin and it analogues act as antibacterial polypeptides.  Peptide
CC   analogues are based on an antibacterial peptide isolated from the
CC   helmet crab intrahemocyte fine granule fraction.  They show anti-
CC   bacterial activity against gram positive and gram negative microbes
CC   and fungi.  These polypeptides are useful as antibacterial agents,
CC   germicides or as a preservative effective against various microbes.
CC   They are also thought to have wound healing properties.  See also
CC   AAR96130-34.
XX
SQ   Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;


  Query Match             100.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.4;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGTAAAACGACGGCCAGT 18
          ||||||||||||||||||
Db      1 tgtaaaacgacggccagt 18


RESULT   8
AAT86529
ID   AAT86529 standard; DNA; 18 BP.
XX
AC   AAT86529;
XX
DT   05-JUN-1998  (first entry)
XX
DE   5'-Terminal amine linked oligonucleotide.
XX
KW   Non-fluorescent label; ligand pair; detection; tag; potentiometry;
KW   cleavage; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag= a
FT                   /note= "5'-hexylamine-thymine"
XX
PN   WO9727327-A2.
XX
PD   31-JUL-1997.
XX
PF   23-JAN-1997;   97WO-US01070.
XX
PR   21-MAR-1996;   96US-0015402.
PR   23-JAN-1996;   96US-0010436.
XX
PA   (DARW-) DARWIN MOLECULAR CORP.
XX
PI   Howbert JJ,  Mulligan JT,  Tabone JC,  Van Ness J;
XX
DR   WPI; 1997-393711/36.
XX
PT   Detection of ligand pair binding and analysis of gene expression -
PT   using tags which are detectable by non-fluorescent spectrometry or
PT   potentiometry
XX
PS   Example 4; Page 99; 147pp; English.
XX
CC   This oligonucleotide was used in the preparation of tagged M13 sequence
CC   primers. The invention relates to a method for detecting the binding of
CC   a first member to a second member of a ligand pair. It comprises: (a)
CC   combining a set of first tagged members with a biological sample (which
CC   may contain one or more second members) for a time sufficient to permit
CC   binding of a first member to a second member, where the tag is
CC   correlative with a particular first member and detectable by non-
CC   fluorescent spectrometry or potentiometry; (b) separating bound first
CC   and second members from unbound members; (c) cleaving the tag from the
CC   tagged first member; and (d) detecting the tag by non-fluorescent
CC   spectrometry or potentiometry, and thus detecting the binding of the
CC   first member to the second member. Analysing the pattern of gene
CC   expression from a selected biological sample comprises: (a) exposing
CC   nucleic acids from a biological sample; (b) combining the exposed
CC   nucleic acids with one or more tagged nucleic acid probes for a time
CC   sufficient for the probes to hybridise to the nucleic acids, where the
CC   tag is correlative with a particular nucleic acid probe and detectable
CC   by non-fluorescent spectrometry or potentiometry; (c) separating
CC   hybridised probes from unhybridised probes; (d) cleaving the tag from
CC   the tagged fragment; and (e) detecting the tag by non-fluorescent
CC   spectrometry or potentiometry, and thus determining the pattern of gene
CC   expression of the sample. The methods may be used in a wide variety of
CC   assays, including nucleic acid assays (e.g. for diagnostic purposes),
CC   protein-based assays, gene expression analysis, detection of
CC   microorganisms, detection of specific sequences in nucleic acid, or
CC   detection of mutations.
```

```
XX
SQ   Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;


  Query Match             100.0%;  Score 18;  DB 18;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.4;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTAAAACGACGGCCAGT 18
           ||||||||||||||||||
Db       1 tgtaaaacgacggccagt 18


RESULT   9
AAV06702
ID   AAV06702 standard; DNA; 18 BP.
XX
AC   AAV06702;
XX
DT   21-MAY-1998  (first entry)
XX
DE   Tagged M13 sequence primer for detection of nucleic acid molecules.
XX
KW   Nucleic acid analysis; tag; linker; M13 sequence primer; PCR;
KW   non-fluorescent spectrometry; potentiometry; detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "5'-hexylamine-Thymine"
XX
PN   WO9727325-A2.
XX
PD   31-JUL-1997.
XX
PF   23-JAN-1997;   97WO-US01046.
XX
PR   04-JUN-1996;   96US-0020487.
PR   23-JAN-1996;   96US-0014536.
XX
PA   (DARW-) DARWIN MOLECULAR CORP.
XX
PI   Howbert JJ,  Mulligan JT,  Tabone JC,  Van Ness J;
XX
DR   WPI; 1997-393709/36.
XX
PT   Detection and identification of nucleic acid molecules  - using tags
PT   which may be detected by non-fluorescent spectrometry or
PT   potentiometry
XX
PS   Example 4; Page 94; 129pp; English.
XX
CC   This sequence represents an M13 sequence primer. The invention relates
CC   to a method for determining the identity of a nucleic acid (NA)
CC   molecule which comprises: (a) generating tagged NA molecules from one or
CC   more selected tagged NA molecules, where a tag is correlative with a
CC   particular NA fragment and detectable by non-fluorescent spectrometry or
CC   potentiometry; (b) separating the tagged molecules by size; (c) cleaving
CC   the tag from the tagged molecule; and (d) detecting the tag by non-
CC   fluorescent spectrometry or potentiometry, and thus determining the
CC   identity of the NA molecule. Detecting a selected NA molecule comprises:
CC   (a) combining a tagged NA probe with target NA molecules for a time
CC   sufficient to permit hybridisation of the probe to a complementary
CC   selected target NA sequence, where the tagged NA probe is detectable by
CC   non-fluorescent spectrometry or potentiometry; (b) altering the size of
CC   the hybridised tagged probes, the size of unhybridised probes or target
CC   molecules, or the size of the probe:target hybrids; (c) separating the
CC   tagged probes by size; (d) cleaving the tag from the tagged probe; and
CC   (e) detecting the tag by non-fluorescent spectrometry or potentiometry,
CC   and thus detecting the selected NA molecule.
XX
SQ   Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;


  Query Match             100.0%;  Score 18;  DB 18;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.4;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTAAAACGACGGCCAGT 18
           ||||||||||||||||||
Db       1 tgtaaaacgacggccagt 18


RESULT  10
AAV06703
ID   AAV06703 standard; DNA; 18 BP.
XX
AC   AAV06703;
XX
DT   22-MAY-1998  (first entry)
XX
DE   5'-Terminal amine linked oligonucleotide DMO 767.
XX
KW   DNA sequencing; tag; mass spectrometry; non-fluorescent spectrometry;
KW   potentiometry; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "5'-hexylamine-Thymine"
XX
PN   WO9727331-A2.
XX
PD   31-JUL-1997.
XX
PF   23-JAN-1997;   97WO-US01304.
XX
PR   23-JAN-1996;   96US-0589260.
PR   23-JAN-1996;   96US-0010462.
XX
PA   (DARW-) DARWIN MOLECULAR CORP.
XX
PI   Howbert JJ,  Mulligan JT,  Tabone JC,  Van Ness J;
XX
DR   WPI; 1997-393715/36.
XX
PT   Determination of nucleic acid sequences  - using tags which are
PT   detectable by non-fluorescent spectrometry or potentiometry
XX
PS   Example 5; Page 111; 182pp; English.
XX
CC   This sequence represents an oligonucleotide shown in the specification.
CC   The invention relates to compounds and a method for determining the
CC   sequence of a nucleic acid molecule. The method comprises: (a) generating
CC   tagged nucleic acid fragments which are complementary to a selected
CC   target nucleic acid, where a tag is correlative with a particular
CC   nucleotide and detectable by non-fluorescent spectrometry or
CC   potentiometry; (b) separating the tagged fragments by sequential length;
CC   (c) cleaving the tags from the tagged fragments; and (d) detecting the
CC   tags by non-fluorescent spectrometry or potentiometry, and from this
CC   determining the sequence. The methods may be used e.g. for determining
CC   the sequences of nucleic acid molecules. They may be used for
CC   determination of multiple nucleic acid sequences simultaneously. The
CC   methods allow sequencing to be performed with enhanced speed and
CC   sensitivity.
XX
SQ   Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;


  Query Match             100.0%;  Score 18;  DB 18;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.4;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy      1 TGTAAAACGACGGCCAGT 18
          ||||||||||||||||||
Db      1 tgtaaaacgacggccagt 18


RESULT 11
AAV12872
ID   AAV12872 standard; DNA; 18 BP.
XX
AC   AAV12872;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Primer M13-21 for M13 DNA sequence.
XX
KW   Energy transfer dye; donor dye; acceptor dye; oligonucleotide labelling;
KW   nucleic acid sequencing; fluorescence intensity; M13; PCR primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag= a
FT                   /note= "modified with aminohexyl linkage, to enable
FT                          attachment to energy transfer dye"
XX
PN   EP805190-A2.
XX
PD   05-NOV-1997.
XX
PF   02-MAY-1997;   97EP-0303039.
XX
PR   04-OCT-1996;   96US-0726462.
PR   03-MAY-1996;   96US-0642330.
XX
PA   (PEKE ) PERKIN-ELMER CORP.
XX
PI   Lee LG,  Rosenblum B,  Spurgeon SL;
XX
DR   WPI; 1997-529051/49.
XX
PT   Fluorescent energy transfer dyes - useful for labelling
PT   dideoxynucleotides, oligonucleotides, etc.
XX
PS   Example 5; Page 55; 79pp; English.
XX
CC   This sequence represents a primer for identifying the M13 sequence shown
CC   in AAV12872. This sequence is labelled with a dye of the invention. The
CC   dye is an energy transfer dyes of formula D-R21-Z1-CO-R22-R28-A (I),
CC   where: D is a donor dye that absorbs light at a first wavelength and
CC   emits excitation energy in response; A is an acceptor dye that absorbs
CC   the excitation energy from D and fluoresces at a second wavelength in
CC   response; Z1 = NH, S or O; R21 = 1-5C alkylene; R22 = an alkene, diene
CC   or alkyne group, an unsaturated 5- or 6-membered ring or a fused ring
CC   structure; R28 = a group which includes a functionality to attach the
CC   linker to the acceptor dye. R28 is especially R29-Z2-CO, where R29 =
CC   1-5C alkylene and Z2 = NH, S or O. The dyes are used for labelling
CC   nucleosides, nucleoside mono-, di- and triphosphates, oligonucleotides
CC   and oligonucleotide analogues, especially for labelling oligonucleotide
CC   primers or dideoxynucleotides used for nucleic acid sequencing. The dyes
CC   give greater fluorescence intensities than the acceptor dyes alone.
XX
SQ   Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;


  Query Match             100.0%;  Score 18;  DB 18;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.4;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGTAAAACGACGGCCAGT 18
          ||||||||||||||||||
Db      1 tgtaaaacgacggccagt 18


RESULT 12
AAV04321
ID   AAV04321 standard; DNA; 18 BP.
XX
AC   AAV04321;
XX
DT   20-APR-1998  (first entry)
XX
DE   Primer used in preparation of osteoprotegrin products.
XX
KW   Osteoprotegerin; antibody; diagnosis; affinity purification;
KW   recombinant production; transgenic animal; treatment; prevention;
KW   antisense oligonucleotide; probe; detection; screening;
KW   bone disease; osteoporosis; Paget's disease; hypercalcaemia;
KW   hyperparathyroidism; rheumatoid arthritis; osteomyelitis;
KW   osteolytic metastasis; periodontal bone loss; bone necrosis;
KW   osteopaenia; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   DE19654610-A1.
XX
PD   26-JUN-1997.
XX
PF   20-DEC-1996;   96DE-1054610.
XX
PR   03-SEP-1996;   96US-0706945.
PR   22-DEC-1995;   95US-0577788.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ,  Calzone FJ,  Lacey DL,  Chang MS;
XX
DR   WPI; 1997-334271/31.
XX
PT   Nucleic acid encoding osteoprotegerin - useful for treatment of
PT   diseases involving excessive bone loss, e.g. osteoporosis
XX
PS   Example 1; Page 14; 182pp; German.
XX
CC   The present sequence is a primer, which was used in the preparation
CC   of osteoprotegerin (OPG) products. Anti-OPG antibodies can be used
CC   in OPG diagnostic assays, and as affinity purification materials.
CC   The OPG cDNA can be used to express recombinant OPG and to generate
CC   transgenic animals. It can also be used to regulate the level of
CC   OPG in mammals, specifically to increase OPG levels, however the
CC   use of antisense sequences is also contemplated. Fragments of the
CC   cDNA can be used as probes to detect OPG expressing cells and
CC   tissue, and to screen cDNA libraries for related sequences. OPG can
CC   be used to treat or prevent bone diseases, specifically excessive
CC   bone loss, e.g. osteoporosis, Paget's disease, hypercalcaemia,
CC   hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
CC   osteolytic metastases, periodontal bone loss, bone necrosis and
CC   osteopaenia.
XX
SQ   Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;


  Query Match             100.0%;  Score 18;  DB 18;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.4;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGTAAAACGACGGCCAGT 18
          ||||||||||||||||||
Db      1 tgtaaaacgacggccagt 18


RESULT 13
AAT89488
ID   AAT89488 standard; DNA; 18 BP.
XX
```

```
AC   AAT89488;
XX
DT   20-JAN-1998  (first entry)
XX
DE   Human recombinant phosphorylated beta-casein gene PCR primer.
XX
KW   Human beta-casein; hBC; phosphorylation; recombinant;
KW   PCR primer; Haemophilus influenzae; adhesion; inhibition;
KW   infant formula; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9717449-A1.
XX
PD   15-MAY-1997.
XX
PF   06-NOV-1996;   96WO-US17729.
XX
PR   06-NOV-1995;   95US-0554135.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Baxter JH,  Hansson L,  Hards RG,  Mukerji P,  Thurmond JM;
XX
DR   WPI; 1997-281038/25.
XX
PT   Production of recombinant phosphorylated human beta-casein - using
PT   plasmid comprising promoter, sequence encoding beta-casein and
PT   sequence for phosphorylating kinase
XX
PS   Disclosure; Page 34; 51pp; English.
XX
CC   This primer is used in PCR amplification for producing beta-casein in
CC   E. coli. The amplified fragment after purification is cloned in the
CC   expression vector pET-26b and beta-casein in E. coli is produced after
CC   further expression and recombination techniques. Such extra cellular
CC   localisation eases the purification process of the phosphorylated human
CC   beta-casein (hBC). The phosphorylated hBC has the same bioactivity as
CC   native hBC as shown by its ability to inhibit the adhesion of
CC   H. influenza to human pharyngeal cells. The recombinant phosphorylated
CC   hBC can be used in liquid nutritional products, particularly in an
CC   infant formula.
CC   Note: This sequence designated as SEQ.ID.No.3 in the sequence listing
CC   differs from the sequence described as SEQ.ID. No.3 in Example 5
CC   (see AAT66778).
XX
SQ   Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;

  Query Match             100.0%;  Score 18;  DB 18;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.4;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTAAAACGACGGCCAGT 18
           ||||||||||||||||||
Db       1 tgtaaaacgacggccagt 18


RESULT  14
AAT89489
ID   AAT89489 standard; DNA; 18 BP.
XX
AC   AAT89489;
XX
DT   20-JAN-1998  (first entry)
XX
DE   Human recombinant phosphorylated beta-casein gene PCR primer.
XX
KW   Human beta-casein; hBC; phosphorylation; recombinant;
KW   PCR primer; Haemophilus influenzae; adhesion; inhibition;
KW   otitis media; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9717085-A2.
XX
PD   15-MAY-1997.
XX
PF   06-NOV-1996;   96WO-US17860.
XX
PR   06-NOV-1995;   95US-0552529.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Anderson SN,  Baxter JH,  Hards RG,  Harvey LA;
PI   Leonard AE,  Mukerji P,  Thurmond JM,  Hansson LB;
XX
DR   WPI; 1997-280800/25.
XX
PT   Inhibiting attachment of H. influenzae to human cells  - uses
PT   recombinant phosphorylated beta-casein, protects human infants from
PT   otitis media
XX
PS   Disclosure; Page 32; 48pp; English.
XX
CC   This primer is used in PCR amplification for producing beta-casein in
CC   E. coli. The amplified fragment after purification is cloned in the
CC   expression vector pET-26b and beta-casein in E. coli is produced after
CC   further expression and recombination techniques. Such extra cellular
CC   localisation eases the purification process of the phosphorylated human
CC   beta-casein (hBC). The phosphorylated hBC has the same bioactivity as
CC   native hBC as shown by its ability to inhibit the adhesion of
CC   H. influenza to human pharyngeal cells. The recombinant phosphorylated
CC   hBC can be used for inhibiting H. influenzae attachment to (naso)
CC   pharangeal cells and for protecting human infants from otitis media.
CC   Note: This sequence designated as SEQ.ID.No.3 in the sequence listing
CC   differs from the sequence described as SEQ.ID. No.3 in Example 5
CC   (see AAT68821).
XX
SQ   Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;

  Query Match             100.0%;  Score 18;  DB 18;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.4;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTAAAACGACGGCCAGT 18
           ||||||||||||||||||
Db       1 tgtaaaacgacggccagt 18


RESULT  15
AAT88395
ID   AAT88395 standard; DNA; 18 BP.
XX
AC   AAT88395;
XX
DT   29-JAN-1998  (first entry)
XX
DE   Energy transfer fluorescent dye tagged oligonucleotide label.
XX
KW   Energy donor; energy acceptor; energy transfer; identification;
KW   fluorescent dye tagged oligonucleotide; label; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "donor-acceptor fluorophore pair separated
FT                          by six 1',2'-dideoxyribose phosphates (S),
FT                          e.g. 5'-Donor-SSSSSS-T-Acceptor"
XX
PN   WO9711084-A1.
```

XX
PD 27-MAR-1997.
XX
PF 12-AUG-1996; 96WO-US13134.
XX
PR 20-SEP-1995; 95US-0531132.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Glazer AN, Ju J, Mathies RA;
XX
DR WPI; 1997-202806/18.
XX
PT New compounds comprising an energy donor component and an acceptor
PT component - are useful as labels for identifying different nucleic
PT acid sequences in electrophoresis
XX
PS Example; Page 9; 22pp; English.
XX
CC A novel compound comprises an energy donor component (EDC) and an
CC acceptor component (AC), which absorbs energy transferred by the
CC EDC, linked by a backbone comprising sugar phosphate ester monomer
CC linkages with the 1-hydroxyl group being etherified or replaced by
CC a hydrogen. The present sequence, a typical energy transfer
CC fluorescent dye tagged oligonucleotide, was synthesised with
CC donor-acceptor fluorophore pairs separated by six
CC 1',2'-dideoxyribose phosphates. The compound can be used as a label
CC to identify different nucleic acid sequences in electrophoresis
CC separations, and may be prepared using conventional polynucleotide
CC synthetic techniques. When a family of the compounds share a common
CC EDC and spacers, but vary as to the AC, they can be excited at the
CC same wavelength, but exhibit widely spaced emission wavelengths.
XX
SQ Sequence 18 BP; 6 A; 4 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTAAAACGACGGCCAGT 18
||||||||||||||||||
Db 1 tgtaaaacgacggccagt 18

Search completed: August 1, 2002, 09:37:28
Job time: 6764 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 09:30:47 ; Search time 87.24 Seconds
(without alignments)
50.681 Million cell updates/sec

Title: US-10-014-743-2
Perfect score: 18
Sequence: 1 TGTAAAACGACGGCCAGT 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	100.0	18	1	US-08-045-758B-1	Sequence 1, Appli
2	18	100.0	18	1	US-08-286-889-40	Sequence 40, Appl
3	18	100.0	18	1	US-08-494-216-1	Sequence 1, Appli
4	18	100.0	18	1	US-08-471-601-2	Sequence 2, Appli
5	18	100.0	18	1	US-08-474-556-2	Sequence 2, Appli
6	18	100.0	18	1	US-08-554-642-3	Sequence 3, Appli
7	18	100.0	18	1	US-08-485-618-40	Sequence 40, Appl
8	18	100.0	18	1	US-08-351-899-2	Sequence 2, Appli
9	18	100.0	18	1	US-08-479-382-2	Sequence 2, Appli
10	18	100.0	18	1	US-08-362-652-40	Sequence 40, Appl
11	18	100.0	18	1	US-08-505-509-3	Sequence 3, Appli
12	18	100.0	18	1	US-08-470-354-2	Sequence 2, Appli
13	18	100.0	18	1	US-08-479-383-2	Sequence 2, Appli
14	18	100.0	18	1	US-08-512-681-26	Sequence 26, Appl
15	18	100.0	18	1	US-08-726-462B-2	Sequence 2, Appli
16	18	100.0	18	1	US-08-554-135-3	Sequence 3, Appli
17	18	100.0	18	1	US-08-605-672-40	Sequence 40, Appl
18	18	100.0	18	2	US-08-482-293A-40	Sequence 40, Appl
19	18	100.0	18	2	US-08-943-363-40	Sequence 40, Appl
20	18	100.0	18	2	US-08-479-041-2	Sequence 2, Appli
21	18	100.0	18	2	US-08-491-690A-3	Sequence 3, Appli
22	18	100.0	18	2	US-08-710-330A-7	Sequence 7, Appli
23	18	100.0	18	2	US-08-540-228-1	Sequence 1, Appli
24	18	100.0	18	2	US-08-505-617-11	Sequence 11, Appl
25	18	100.0	18	2	US-08-642-330-2	Sequence 2, Appli
26	18	100.0	18	2	US-08-432-871C-32	Sequence 32, Appl
27	18	100.0	18	2	US-08-751-189-9	Sequence 9, Appli
28	18	100.0	18	2	US-08-951-648-28	Sequence 28, Appl
29	18	100.0	18	2	US-08-964-725-9	Sequence 9, Appli
30	18	100.0	18	2	US-08-554-137-3	Sequence 3, Appli
31	18	100.0	18	2	US-09-046-203-2	Sequence 2, Appli
32	18	100.0	18	2	US-09-018-170-11	Sequence 11, Appl
33	18	100.0	18	2	US-08-948-364-1	Sequence 1, Appli
34	18	100.0	18	2	US-09-060-836-9	Sequence 9, Appli
35	18	100.0	18	2	US-08-715-461-1	Sequence 1, Appli
36	18	100.0	18	2	US-08-815-448-1	Sequence 1, Appli
37	18	100.0	18	2	US-08-890-980-85	Sequence 85, Appl
38	18	100.0	18	3	US-08-589-939-70	Sequence 70, Appl
39	18	100.0	18	3	US-08-974-022-10	Sequence 10, Appl
40	18	100.0	18	3	US-08-890-979-74	Sequence 74, Appl
41	18	100.0	18	3	US-08-873-470-1	Sequence 1, Appli
42	18	100.0	18	3	US-09-147-550-114	Sequence 114, App
43	18	100.0	18	3	US-09-032-894-85	Sequence 85, Appl
44	18	100.0	18	3	US-09-071-710-20	Sequence 20, Appl
45	18	100.0	18	3	US-09-174-437-28	Sequence 28, Appl

ALIGNMENTS

```
RESULT   1
US-08-045-758B-1
; Sequence 1, Application US/08045758B
; Patent No. 5451663
;  GENERAL INFORMATION:
;    APPLICANT:  Kang, Hee Chol
;    APPLICANT:  Haugland, Richard P.
;    TITLE OF INVENTION:  Long Wavelength Chemically Reactive Dipyrrometheneboron
;    TITLE OF INVENTION:  Difluoride Dyes and Conjugates.
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Molecular Probes, Inc.
;      STREET:  4849 Pitchford Avenue
;      CITY:  Eugene
;      STATE:  Oregon
;      COUNTRY:  USA
;      ZIP:  97402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  MS-DOS 6.0
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/045,758B
;      FILING DATE:  04/08/93
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/786,767
;      FILING DATE:  11/01/91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Helfenstein, Allegra J.
;      REGISTRATION NUMBER:  34,179
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (503)465-8300
;      TELEFAX:  (503)344-6504
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 bases
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  Other nucleic acid
;      DESCRIPTION:  A 5'-amine-derivatized oligonucleotide prepared by automated
;      DESCRIPTION:  solid phase synthesis.
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
US-08-045-758B-1

  Query Match                 100.0%;  Score 18;  DB 1;  Length 18;
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  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTAAAACGACGGCCAGT 18
           ||||||||||||||||||
Db       1 TGTAAAACGACGGCCAGT 18


RESULT   2
US-08-286-889-40
; Sequence 40, Application US/08286889
; Patent No. 5470953
;  GENERAL INFORMATION:
;    APPLICANT:  Gallatin, W. Mich
;    APPLICANT:  Van der Vieren, Monica
;    TITLE OF INVENTION:  No. 5470953el Human  2 Integrin Alpha Subunit
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  233 South Wacker Drive, 6300 Sear Tower
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/286,889
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/173,497
;      FILING DATE:  23-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams Jr., Joseph A.
;      REGISTRATION NUMBER:  P38,659
;      REFERENCE/DOCKET NUMBER:  27866/32168
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;      TELEFAX:  312-474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-286-889-40


  Query Match             100.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTAAAACGACGGCCAGT 18
           ||||||||||||||||||
Db       1 TGTAAAACGACGGCCAGT 18


RESULT   3
US-08-494-216-1
; Sequence 1, Application US/08494216
; Patent No. 5614386
;  GENERAL INFORMATION:
;    APPLICANT:  METZKER, MICHAEL L.
;    APPLICANT:  GIBBS, RICHARD A.
;    TITLE OF INVENTION:  ALTERNATIVE DYE-LABELED PRIMERS FOR
;    TITLE OF INVENTION:  AUTOMATED DNA SEQUENCING
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FULBRIGHT & JAWORSKI L.L.P.
;      STREET:  1301 MCKINNEY, SUITE 5100
;      CITY:  HOUSTON
;      STATE:  TEXAS
;      COUNTRY:  USA
;      ZIP:  77010
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/494,216
;      FILING DATE:  23-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BRASHEARS-MACATEE, SARAH J.
;      REGISTRATION NUMBER:  38,087
;      REFERENCE/DOCKET NUMBER:  D-5776
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713-651-5151
;      TELEFAX:  713-651-5246
;      TELEX:  76-2829
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    POSITION IN GENOME:
;      UNITS:  18 bp
US-08-494-216-1


  Query Match             100.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTAAAACGACGGCCAGT 18
           ||||||||||||||||||
Db       1 TGTAAAACGACGGCCAGT 18


RESULT   4
US-08-471-601-2
; Sequence 2, Application US/08471601
; Patent No. 5689049
;  GENERAL INFORMATION:
;    APPLICANT:  CIGAN, Andrew M.
;    APPLICANT:  ALBERTSEN, Marc C.
;    TITLE OF INVENTION:  Reversible Nuclear Genetic System For
;    TITLE OF INVENTION:  Male Sterility In Transgenic Plants
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/471,601
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
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```
;      APPLICATION NUMBER:  US 08/351,899
;      FILING DATE:  08-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  33229/341/PIHI
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-471-601-2


  Query Match           100.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 0.38;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTAAAACGACGGCCAGT 18
           ||||||||||||||||||
Db       1 TGTAAAACGACGGCCAGT 18


RESULT   5
US-08-474-556-2
; Sequence 2, Application US/08474556
; Patent No. 5689051
;  GENERAL INFORMATION:
;    APPLICANT:  CIGAN, Andrew M.
;    APPLICANT:  ALBERTSEN, Marc C.
;    TITLE OF INVENTION:  Reversible Nuclear Genetic System For
;    TITLE OF INVENTION:  Male Sterility In Transgenic Plants
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,556
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/351,899
;      FILING DATE:  08-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  33229/329/PIHI
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-474-556-2


  Query Match           100.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 0.38;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTAAAACGACGGCCAGT 18
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Db       1 TGTAAAACGACGGCCAGT 18


RESULT   6
US-08-554-642-3
; Sequence 3, Application US/08554642
; Patent No. 5710044
;  GENERAL INFORMATION:
;    APPLICANT:  Mukerji, P.
;    APPLICANT:  Thurmond, J.
;    APPLICANT:  Hansson, L.
;    APPLICANT:  Baxter, J.
;    APPLICANT:  Hards, R.
;    TITLE OF INVENTION:  A Plasmid For Expressing Modified
;    TITLE OF INVENTION:  Recombinant Proteins in a Bacterial
;    TITLE OF INVENTION:  System
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Donald O. Nickey
;      ADDRESSEE:  ROSS Products Division
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  625 Cleveland Avenue
;      CITY:  Columbus
;      STATE:  Ohio
;      COUNTRY:  United States of America
;      ZIP:  43215
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS Version 6.21
;      SOFTWARE:  WordPerfect Version 6.0a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/554,642
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/395,239
;      FILING DATE:  27-FEB-1995
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (614) 624-7080
;      TELEFAX:  (614) 624-3074
;      TELEX:  No. 5710044e
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  Nucleic acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  DNA
US-08-554-642-3


  Query Match           100.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 0.38;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTAAAACGACGGCCAGT 18
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Db       1 TGTAAAACGACGGCCAGT 18


RESULT   7
US-08-485-618-40
; Sequence 40, Application US/08485618
; Patent No. 5728533
;  GENERAL INFORMATION:
;    APPLICANT:  Gallatin, W. Michael
```

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;    APPLICANT:  Van der Vieren, Monica
;    TITLE OF INVENTION:  No. 5728533el Human  2 Integrin Alpha Subunit
;    NUMBER OF SEQUENCES:  103
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  233 South Wacker Drive, 6300 Sear Tower
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,618
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/173,497
;      FILING DATE:  23-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/286,889
;      FILING DATE:  5-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/362,652
;      FILING DATE:  21-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams Jr., Joseph A.
;      REGISTRATION NUMBER:  38,659
;      REFERENCE/DOCKET NUMBER:  27866/32797
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;      TELEFAX:  312-474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-485-618-40


  Query Match             100.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTAAAACGACGGCCAGT 18
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Db       1 TGTAAAACGACGGCCAGT 18


RESULT   8
US-08-351-899-2
; Sequence 2, Application US/08351899
; Patent No. 5750868
;  GENERAL INFORMATION:
;    APPLICANT:  CIGAN, Andrew M.
;    APPLICANT:  ALBERTSEN, Marc C.
;    TITLE OF INVENTION:  Reversible Nuclear Genetic System For
;    TITLE OF INVENTION:  Male Sterility In Transgenic Plants
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/351,899
;      FILING DATE:  08-DEC-1994
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  33229/208/PIHI
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-351-899-2


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  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTAAAACGACGGCCAGT 18
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Db       1 TGTAAAACGACGGCCAGT 18


RESULT   9
US-08-479-382-2
; Sequence 2, Application US/08479382
; Patent No. 5763243
;  GENERAL INFORMATION:
;    APPLICANT:  CIGAN, Andrew M.
;    APPLICANT:  ALBERTSEN, Marc C.
;    TITLE OF INVENTION:  Reversible Nuclear Genetic System For
;    TITLE OF INVENTION:  Male Sterility In Transgenic Plants
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/479,382
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/351,899
;      FILING DATE:  08-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  33229/339/PIHI
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
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;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-479-382-2


  Query Match             100.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTAAAACGACGGCCAGT 18
           ||||||||||||||||||
Db       1 TGTAAAACGACGGCCAGT 18


RESULT  10
US-08-362-652-40
; Sequence 40, Application US/08362652
; Patent No. 5766850
;  GENERAL INFORMATION:
;    APPLICANT:  Gallatin, W. Michael
;    APPLICANT:  Van der Vieren, Monica
;    TITLE OF INVENTION:  No. 5766850el Human  2 Integrin Alpha Subunit
;    NUMBER OF SEQUENCES:  93
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  233 South Wacker Drive, 6300 Sear Tower
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/362,652
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/173,497
;      FILING DATE:  23-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/286,889
;      FILING DATE:  5-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams Jr., Joseph A.
;      REGISTRATION NUMBER:  38,659
;      REFERENCE/DOCKET NUMBER:  27866/32391
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;      TELEFAX:  312-474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-362-652-40


  Query Match             100.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTAAAACGACGGCCAGT 18
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Db       1 TGTAAAACGACGGCCAGT 18


RESULT  11
US-08-505-509-3
; Sequence 3, Application US/08505509
; Patent No. 5776680
;  GENERAL INFORMATION:
;    APPLICANT:  Liebowitz, Michael J.
;    APPLICANT:  Liu, Yong
;    TITLE OF INVENTION:  Diagnostic Probes for
;    TITLE OF INVENTION:  Pneumocystis Carinii
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Richard R. Muccino
;      STREET:  P.O. Box 1267
;      CITY:  Princeton
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  08551
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/505,509
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/298,087
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/922,987
;      FILING DATE:  30-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Muccino, Richard R.
;      REGISTRATION NUMBER:  32,538
;      REFERENCE/DOCKET NUMBER:  UMD1-009
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (609) 466-3407
;      TELEFAX:  (609) 466-2760
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-505-509-3


  Query Match             100.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTAAAACGACGGCCAGT 18
           ||||||||||||||||||
Db       1 TGTAAAACGACGGCCAGT 18


RESULT  12
US-08-470-354-2
; Sequence 2, Application US/08470354
; Patent No. 5792853
;  GENERAL INFORMATION:
;    APPLICANT:  CIGAN, Andrew M.
;    APPLICANT:  ALBERTSEN, Marc C.
;    TITLE OF INVENTION:  Reversible Nuclear Genetic System For
;    TITLE OF INVENTION:  Male Sterility In Transgenic Plants
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
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;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,354
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/351,899
;      FILING DATE:  08-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  33229/337/PIHI
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-470-354-2


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  Best Local Similarity  100.0%;  Pred. No. 0.38;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGTAAAACGACGGCCAGT 18
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Db      1 TGTAAAACGACGGCCAGT 18


RESULT  13
US-08-479-383-2
; Sequence 2, Application US/08479383
; Patent No. 5795753
;  GENERAL INFORMATION:
;    APPLICANT:  CIGAN, Andrew M.
;    APPLICANT:  ALBERTSEN, Marc C.
;    TITLE OF INVENTION:  Reversible Nuclear Genetic System For
;    TITLE OF INVENTION:  Male Sterility In Transgenic Plants
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/479,383
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/351,899
;      FILING DATE:  08-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  33229/340/PIHI
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-479-383-2


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  Best Local Similarity  100.0%;  Pred. No. 0.38;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGTAAAACGACGGCCAGT 18
          ||||||||||||||||||
Db      1 TGTAAAACGACGGCCAGT 18


RESULT  14
US-08-512-681-26
; Sequence 26, Application US/08512681
; Patent No. 5795976
;  GENERAL INFORMATION:
;    APPLICANT:  Oefner, Peter J.
;    APPLICANT:  Underhill, Peter A.
;    TITLE OF INVENTION:  Detection of DNA Heteroduplex Molecules
;    TITLE OF INVENTION:  by Denaturing High Performance Liquid Chromatography and
;    TITLE OF INVENTION:  Methods for Comparative Sequencing
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Ave., Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/512,681
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Evans, Susan T.
;      REGISTRATION NUMBER:  38,443
;      REFERENCE/DOCKET NUMBER:  8600-0155
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  439-MER FORWARD PRIMER
US-08-512-681-26


  Query Match           100.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 0.38;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGTAAAACGACGGCCAGT 18
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Db      1 TGTAAAACGACGGCCAGT 18


RESULT  15
US-08-726-462B-2
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; Sequence 2, Application US/08726462B
; Patent No. 5800996
;  GENERAL INFORMATION:
;    APPLICANT:  Perkin-Elmer Corporation, Applied Biosystems
;    APPLICANT:  Division
;    TITLE OF INVENTION:  ENERGY TRANSFER DYES WITH ENHANCED
;    TITLE OF INVENTION:  FLUORESCENCE
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David J. Weitz, Wilson Sonsini Goodrich
;      ADDRESSEE:  & Rosati
;      STREET:  650 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1050
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Microsoft Windows 3.1/DOS 5.0
;      SOFTWARE:  Wordperfect for windows 6.0,
;      SOFTWARE:  ASCII (DOS) TEXT format
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/726,462B
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/642,330
;      FILING DATE:  May 3, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/672,196
;      FILING DATE:  June 27, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David J. Weitz
;      REGISTRATION NUMBER:  38,362
;      REFERENCE/DOCKET NUMBER:  PELM4304
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 493-9300
;      TELEFAX:  (415) 493-6811
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-726-462B-2


  Query Match           100.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTAAAACGACGGCCAGT 18
           ||||||||||||||||||
Db       1 TGTAAAACGACGGCCAGT 18


Search completed: August  1, 2002, 09:30:48
Job time: 6609 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 08:39:40 ; Search time 2971.21 Seconds
(without alignments)
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Title: US-10-014-743-2
Perfect score: 18
Sequence: 1 TGTAAAACGACGGCCAGT 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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6: em_estpl:*
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8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	18	100.0	73	9	AA680645	AA680645 LmFrAm009
c 2	18	100.0	88	10	BI938357	BI938357 de42a01.y
c 3	18	100.0	89	10	N28043	N28043 EST000247 S
4	18	100.0	90	9	AJ239924	AJ239924 AJ239924
c 5	18	100.0	92	10	N28040	N28040 EST000177 S
c 6	18	100.0	94	10	BI845735	BI845735 fs96c02.x
c 7	18	100.0	96	10	R29179	R29179 F1-287D 22
c 8	18	100.0	99	10	T10982	T10982 hbc297 Huma
c 9	18	100.0	100	9	AA952864	AA952864 SMTBADA00
c 10	18	100.0	100	9	AA098627	AA098627 SMTBADAMS
c 11	18	100.0	100	9	AW113079	AW113079 MC7322 mo
12	18	100.0	100	9	AW754394	AW754394 CM0-CT034
c 13	18	100.0	100	9	AW812014	AW812014 RC6-ST017
c 14	18	100.0	100	9	AW812016	AW812016 RC6-ST017
15	18	100.0	100	10	BF901653	BF901653 RC4-MT016
16	18	100.0	100	12	BH234794	BH234794 MEAA_B03.
c 17	18	100.0	102	9	AA741768	AA741768 LmLv39p3/
c 18	18	100.0	103	9	AU180326	AU180326 AU180326
19	18	100.0	103	9	BE079941	BE079941 RC4-BT062
20	18	100.0	105	9	AW754393	AW754393 CM0-CT034
c 21	18	100.0	108	10	BI716021	BI716021 ic64f02.y
c 22	18	100.0	109	10	N28049	N28049 EST000286 S
c 23	18	100.0	110	9	AA728161	AA728161 LmLv39p7/
c 24	18	100.0	110	9	AA741956	AA741956 LmLv39p3/
c 25	18	100.0	113	9	AA728380	AA728380 LmLv39p7/
26	18	100.0	113	9	AW749048	AW749048 CM0-BT032
27	18	100.0	113	9	AW809021	AW809021 MR1-ST011
28	18	100.0	114	9	AW809014	AW809014 MR1-ST011
29	18	100.0	115	9	AW809013	AW809013 MR1-ST011
30	18	100.0	117	9	AI940435	AI940435 CM0-CT005
31	18	100.0	117	9	AW062733	AW062733 CM0-CT010
c 32	18	100.0	117	9	BE079985	BE079985 RC4-BT062
c 33	18	100.0	118	9	AA804151	AA804151 SMTBADA00
34	18	100.0	118	9	AW855817	AW855817 RC1-CT027
c 35	18	100.0	119	9	AW750572	AW750572 RC0-CN002
c 36	18	100.0	120	9	AA864147	AA864147 SMTBSOA00
c 37	18	100.0	121	10	BI675749	BI675749 dag55c02.
c 38	18	100.0	122	10	N28034	N28034 EST000119 S
c 39	18	100.0	122	12	BH240653	BH240653 ATXQA87TR
c 40	18	100.0	125	12	BH243317	BH243317 AUIHE80TR
c 41	18	100.0	125	12	BH471635	BH471635 BOGDO75TR
c 42	18	100.0	126	9	AA283326	AA283326 RTH083 HT
43	18	100.0	126	12	BH240234	BH240234 AUINC60TR
c 44	18	100.0	127	10	BM129856	BM129856 pb14b04.y
45	18	100.0	128	9	AW845527	AW845527 MR1-CT005

ALIGNMENTS

RESULT 1
AA680645/c
LOCUS AA680645 73 bp mRNA linear EST 09-DEC-1998
DEFINITION LmFrAm0099 Leishmania major Amastigote Lambda Zap II library
Leishmania major cDNA clone H02 5', mRNA sequence.
ACCESSION AA680645
VERSION AA680645.1 GI:2662650
KEYWORDS EST.
SOURCE Leishmania major.
ORGANISM Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Leishmania.
REFERENCE 1 (bases 1 to 73)
AUTHORS Norrish,A.R., Dyall,S.D., Smith,D.F. and Blackwell,J.M.
TITLE Analysis of Leishmania Major Amastigote Expressed Sequence Tags
JOURNAL Unpublished (1997)
COMMENT Contact: Blackwell JM
Cambridge Institute for Medical Research
Wellcome Trust/MRC Building, Addenbrooke's Hospital, Hills Road,
Cambridge CB2 2XY, UK
Tel: 01223 336 143
Fax: 01223 331 206
Email: jmb37@cus.cam.ac.uk
PCR PRimers
FORWARD: GTAAAACGACGGCCAGT
BACKWARD: GGAAACAGCTATGACCATG
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 72.
FEATURES Location/Qualifiers
source 1. .73
/organism="Leishmania major"
/strain="Friedlin"
/db_xref="taxon:5664"
/clone="H02"
/clone_lib="Leishmania major Amastigote Lambda Zap II
library"
/cell_type="Amastigote"
/note="Vector: Lambda Zap II; Site_1: Xho1; Site_2: Not1"
BASE COUNT 15 a 21 c 18 g 19 t
ORIGIN

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  Query Match             100.0%;  Score 18;  DB 9;  Length 73;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGTAAAACGACGGCCAGT 18
          ||||||||||||||||||
Db     71 TGTAAAACGACGGCCAGT 54


RESULT   2
BI938357/c
LOCUS       BI938357                 88 bp    mRNA    linear   EST 18-OCT-2001
DEFINITION  de42a01.y1 Wellcome CRC pRN3 dorsal lip Xenopus laevis cDNA clone
            IMAGE:3474313 5' similar to TR:Q47522 Q47522 PLASMID PQF50 DNA WITH
            POLYLINKER AND PARTIAL LACZ GENE ;, mRNA sequence.
ACCESSION   BI938357
VERSION     BI938357.1  GI:16252829
KEYWORDS    EST.
SOURCE      African clawed frog.
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1  (bases 1 to 88)
  AUTHORS   Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.
            , Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
            ,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Xenopus EST project, 1999
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: de42a01.x1
            Contact: Sandy Clifton, Ph.D.
            WashU Xenopus EST project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Library constructed by A.M. Zorn (Wellcome/CRC Institute). DNA
            Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: Xenopus clones from this library are available
            through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
            Trace considered overall poor quality
            Seq primer: -40RP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .88
                     /organism="Xenopus laevis"
                     /db_xref="taxon:8355"
                     /clone="IMAGE:3474313"
                     /clone_lib="Wellcome CRC pRN3 dorsal lip"
                     /tissue_type="dorsal lip"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
                     were oligo-dT primed and directionally cloned. Staging
                     according to  Nieuwkoop and Faber. Library was constructed
                     by A.M. Zorn (Wellcome/CRC Institute). "
BASE COUNT       17 a     31 c     17 g     23 t
ORIGIN


  Query Match             100.0%;  Score 18;  DB 10;  Length 88;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGTAAAACGACGGCCAGT 18
          ||||||||||||||||||
Db     21 TGTAAAACGACGGCCAGT 4


RESULT   3
N28043/c
LOCUS       N28043                   89 bp    mRNA    linear   EST 02-JAN-1996
DEFINITION  EST000247 S. mansoni cDNA Schistosoma mansoni cDNA clone
            SMTBADAMS0247SK 5' end similar to M. auratus synaptonemal complex
            DNA, mRNA sequence.
ACCESSION   N28043
VERSION     N28043.1  GI:1145899
KEYWORDS    EST.
SOURCE      Schistosoma mansoni.
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 89)
  AUTHORS   Saber,M.A., Hamied,H., ElYassaki,W.M., Romeih,M., Ahmed,H., Mohareb
            ,M., ElDabaa,I. and Mamdouh,S.
  TITLE     Schistosoma mansoni cDNAs
  JOURNAL   Unpublished (1995)
COMMENT     Contact: M.A. Saber, H. Hamied, W.M. El Yassaki, M. Romeih, H.
            Ahmed, M. Mohareb, I. El Dabaa, S. Mamdouh
            TBRI Biochemistry
            Theodor Bilharz Research Institute
            Imbaba, P.O.Box 12411, Giza, Egypt
            Tel: 202 3128276
            Fax: 202 3121167
            Email: M-Saber@FRCU.EUN.EG
            Seq primer: sk.
FEATURES             Location/Qualifiers
     source          1. .89
                     /organism="Schistosoma mansoni"
                     /strain="Egyptian"
                     /db_xref="taxon:6183"
                     /clone="SMTBADAMS0247SK"
                     /clone_lib="S. mansoni cDNA"
                     /lab_host="E. coli XL Blue1"
                     /note="Vector: pBluescript II SK+; Site_1: EcoR1; Site_2:
                     Xho1; mRNA was purified from adult couples of S. mansoni.
                     cDNA was constructed and cloned simultaneously using
                     vector priming with the pBluescript II SK+ vector. cDNA
                     was directionally synthesized from the EcoR1 site in the
                     vector to the Xho1 site."
BASE COUNT       23 a     23 c     19 g     24 t
ORIGIN


  Query Match             100.0%;  Score 18;  DB 10;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGTAAAACGACGGCCAGT 18
          ||||||||||||||||||
Db     50 TGTAAAACGACGGCCAGT 33


RESULT   4
AJ239924
LOCUS       AJ239924                 90 bp    mRNA    linear   EST 10-AUG-1999
DEFINITION  AJ239924 Aspergillus niger ATCC6275 Aspergillus niger cDNA clone
            AN06F05, mRNA sequence.
ACCESSION   AJ239924
VERSION     AJ239924.1  GI:5443915
KEYWORDS    EST.
SOURCE      Aspergillus niger.
  ORGANISM  Aspergillus niger
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 90)
  AUTHORS   Choi,J.Y., Lee,D.W., Koh,J.S., Kim,J.H., Yang,M.S. and Chae,K.S.
  TITLE     Identification of expressed sequence tags (ESTs) of the highly
            transcribed genes in Aspergillus niger
  JOURNAL   Biotechnol. Lett. 21, 381-384 (1999)
COMMENT     Contact: Chae KS
            Faculty of Biological Sciences
            Chonbuk National University
```

```
          Chonju 561-756, Republic of Korea.
FEATURES             Location/Qualifiers
     source          1. .90
                     /organism="Aspergillus niger"
                     /strain="ATCC6275"
                     /db_xref="taxon:5061"
                     /clone="AN06F05"
                     /clone_lib="Aspergillus niger ATCC6275"
BASE COUNT       21 a     22 c     27 g     20 t
ORIGIN


  Query Match             100.0%;  Score 18;  DB 9;  Length 90;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGTAAAACGACGGCCAGT 18
          ||||||||||||||||||
Db     53 TGTAAAACGACGGCCAGT 70


RESULT   5
N28040/c
LOCUS       N28040                    92 bp    mRNA    linear   EST 02-JAN-1996
DEFINITION  EST000177 S. mansoni cDNA Schistosoma mansoni cDNA clone
            SMTBADAMS0177SK 5' end similar to Homo sapiens cDNA clone CBS-325,
            mRNA sequence.
ACCESSION   N28040
VERSION     N28040.1  GI:1145896
KEYWORDS    EST.
SOURCE      Schistosoma mansoni.
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 92)
  AUTHORS   Saber,M.A., Hamied,H., ElYassaki,W.M., Romeih,M., Ahmed,H., Mohareb
            ,M., ElDabaa,I. and Mamdouh,S.
  TITLE     Schistosoma mansoni cDNAs
  JOURNAL   Unpublished (1995)
COMMENT     Contact: M.A. Saber, H. Hamied, W.M. El Yassaki, M. Romeih, H.
            Ahmed, M. Mohareb, I. El Dabaa, S. Mamdouh
            TBRI Biochemistry
            Theodor Bilharz Research Institute
            Imbaba, P.O.Box 12411, Giza, Egypt
            Tel: 202 3128276
            Fax: 202 3121167
            Email: M-Saber@FRCU.EUN.EG
            Seq primer: sk.
FEATURES             Location/Qualifiers
     source          1. .92
                     /organism="Schistosoma mansoni"
                     /strain="Egyptian"
                     /db_xref="taxon:6183"
                     /clone="SMTBADAMS0177SK"
                     /clone_lib="S. mansoni cDNA"
                     /lab_host="E. coli XL Blue1"
                     /note="Vector: pBluescript II SK+; Site_1: EcoR1; Site_2:
                     Xho1; mRNA was purified from adult couples of S. mansoni.
                     cDNA was constructed and cloned simultaneously using
                     vector priming with the pBluescript II SK+ vector. cDNA
                     was directionally synthesized from the EcoR1 site in the
                     vector to the Xho1 site."
BASE COUNT       20 a     28 c     20 g     24 t
ORIGIN


  Query Match             100.0%;  Score 18;  DB 10;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGTAAAACGACGGCCAGT 18
          ||||||||||||||||||
Db     60 TGTAAAACGACGGCCAGT 43


RESULT   6
BI845735/c
LOCUS       BI845735                  94 bp    mRNA    linear   EST 04-OCT-2001
DEFINITION  fs96c02.x1 Zebrafish neuronal Danio rerio cDNA clone 5077610 3'
            similar to TR:Q47336 Q47336 LACZ-ALPHA PEPTIDE. ;, mRNA sequence.
ACCESSION   BI845735
VERSION     BI845735.1  GI:15958258
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 94)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
            ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
            ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
            Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
            Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
            and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library constructed by S. Lin DNA Sequencing by: Washington
            University Genome Sequencing Center Clone distribution: the
            I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: T7 from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .94
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone="5077610"
                     /clone_lib="Zebrafish neuronal"
                     /sex="mixed"
                     /dev_stage="adult"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: brain; Vector: pBluescript (modified);
                     Site_1: DraIII(Y); Site_2: DRAIII(X); Library is cloned
                     directionally between the DraIII(X) and DraIII(Y) sites
                     and has been amplified. Library constructed by S. Lin. "
BASE COUNT       18 a     32 c     21 g     23 t
ORIGIN


  Query Match             100.0%;  Score 18;  DB 10;  Length 94;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGTAAAACGACGGCCAGT 18
          ||||||||||||||||||
Db     18 TGTAAAACGACGGCCAGT 1


RESULT   7
R29179/c
LOCUS       R29179                    96 bp    mRNA    linear   EST 03-DEC-1999
DEFINITION  F1-287D 22 week old human fetal liver cDNA library Homo sapiens
            cDNA clone F1-287D 5', mRNA sequence.
ACCESSION   R29179
VERSION     R29179.1  GI:1547162
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 96)
  AUTHORS   Choi,S.S., Yun,J.W., Choi,E.K., Cho,Y.G., Sung,Y.C. and Shin,H.S.
  TITLE     Construction of a gene expression profile of a human fetal liver by
            single-pass cDNA sequencing
  JOURNAL   Mamm. Genome 6 (9), 653-657 (1995)
  MEDLINE   96081342
COMMENT     Contact: Hee-Sup Shin
            Developmental Genetics
            Pohang Institute of Science & Technology
            San31, Hyojadong Pohang, 790-784 Republic of Korea
            Tel: 562-279-2291
            Fax: 562-279-2199
            Email: shinhs@vision.postech.ac.kr
            Seq primer: T3 primer.
FEATURES              Location/Qualifiers
     source           1. .96
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="F1-287D"
                      /clone_lib="22 week old human fetal liver cDNA library"
                      /lab_host="XL1-blue MRF'"
                      /note="Vector: pBluescriptII SK(-); Site_1: EcoRI; Site_2:
                      XhoI; The cDNA library made by oligo-dT primed and
                      directionally cloned between 5'ExoR I-XhoI3' sites."
BASE COUNT       24 a      25 c      17 g      26 t       4 others
ORIGIN


  Query Match             100.0%;  Score 18;  DB 10;  Length 96;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTAAAACGACGGCCAGT 18
           ||||||||||||||||||
Db      57 TGTAAAACGACGGCCAGT 40


RESULT   8
T10982/c
LOCUS       T10982                    99 bp    mRNA    linear   EST 29-NOV-1993
DEFINITION  hbc297 Human pancreatic islet Homo sapiens cDNA clone hbc297 5'end,
            mRNA sequence.
ACCESSION   T10982
VERSION     T10982.1  GI:391136
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Takeda,J., Yano,H., Eng,S., Zeng,Y. and Bell,G.I.
  TITLE     A molecular inventory of human pancreatic islets: sequence analysis
            of 1000 cDNA clones
  JOURNAL   Hum. Mol. Genet. 2, 1793-1798 (1993)
  MEDLINE   94108427
COMMENT     Contact: Bell GI or Takeda J
            HHMI
            Univ. of Chicago
            5841 S. Maryland Ave.,MC1028,Chicago IL 60637
            Tel: 3127029116
            Fax: 3127020271
            Email: g-bell@uchicago.edu
            Seq primer: SK primer.
FEATURES              Location/Qualifiers
     source           1. .99
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="hbc297"
                      /clone_lib="Human pancreatic islet"
                      /note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
                      I; mRNA was prepared from normal adult human islets. cDNA
                      was directionally synthesized from the Xho I in the vector
                      to the EcoRI site. cDNA was size fractionated to remove
                      sequences <1000 bp in size."
BASE COUNT       24 a      30 c      20 g      25 t
ORIGIN


  Query Match             100.0%;  Score 18;  DB 10;  Length 99;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTAAAACGACGGCCAGT 18
           ||||||||||||||||||
Db      42 TGTAAAACGACGGCCAGT 25


RESULT   9
AA952864/c
LOCUS       AA952864                  100 bp    mRNA    linear   EST 07-MAY-1998
DEFINITION  SMTBADA000626SK Schistosoma Lambda Zap II Schistosoma mansoni cDNA
            clone SMA626 5', mRNA sequence.
ACCESSION   AA952864
VERSION     AA952864.1  GI:3116456
KEYWORDS    EST.
SOURCE      Schistosoma mansoni.
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Saber,M.A.
  TITLE     Expressed sequence tags from cDNA clones isolated from Schistosoma
            mansoni cDNA libraries
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Saber,MA
            Department of Biochemistery
            Theodor Bilharz Research Institute
            P.O. BOX 30, Imbaba, Giza, Egypt
            Tel: (202) 5402977
            Fax: (202) 5402977
            Email: M_SABER@frcu.eun.eg
            Seq primer: SK primer 'Stratagene'.
FEATURES              Location/Qualifiers
     source           1. .100
                      /organism="Schistosoma mansoni"
                      /strain="Egyptian"
                      /db_xref="taxon:6183"
                      /clone="SMA626"
                      /clone_lib="Schistosoma Lambda Zap II"
                      /sex="Mixed"
                      /dev_stage="Adult"
                      /lab_host="Mus musculus"
                      /note="Vector: Lambda Zap II; Site_1: EcoRI; Site_2: XhoI;
                      Poly adenylated RNA was isolated from adult of  S. mansoni
                      worms "
BASE COUNT       21 a      28 c      27 g      24 t
ORIGIN


  Query Match             100.0%;  Score 18;  DB 9;  Length 100;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTAAAACGACGGCCAGT 18
           ||||||||||||||||||
Db      77 TGTAAAACGACGGCCAGT 60


RESULT  10
AA098627/c
LOCUS       AA098627                  100 bp    mRNA    linear   EST 28-OCT-1996
DEFINITION  SMTBADAMS0626SK S. mansoni cDNA Schistosoma mansoni cDNA clone
            SMTBADAMS0626SK 5' similar to Calothrix D253 genomic clone, mRNA
            sequence.
```

```
ACCESSION   AA098627
VERSION     AA098627.1  GI:1644597
KEYWORDS    EST.
SOURCE      Schistosoma mansoni.
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Saber,M.A., Hamied,H., ElYassaki,W.M., Romeih,M., Ahmed,H., Mohareb
            ,M., ElDabaa,I. and Mamdouh,S.
  TITLE     Schistosoma mansoni cDNAs
  JOURNAL   Unpublished (1995)
COMMENT     Contact: M.A. Saber, H. Hamied, W.M. El Yassaki, M. Romeih, H.
            Ahmed, M. Mohareb, I. El Dabaa, S. Mamdouh
            TBRI Biochemistry
            Theodor Bilharz Research Institute
            Imbaba, P.O.Box 12411, Giza, Egypt
            Tel: 202 3128276
            Fax: 202 3121167
            Email: M-Saber@FRCU.EUN.EG
            Seq primer: sk.
FEATURES            Location/Qualifiers
     source         1. .100
                    /organism="Schistosoma mansoni"
                    /strain="Egyptian"
                    /db_xref="taxon:6183"
                    /clone="SMTBADAMS0626SK"
                    /clone_lib="S. mansoni cDNA"
                    /lab_host="E. coli XL Blue1"
                    /note="Vector: pBluescript II SK+; Site_1: EcoR1; Site_2:
                    Xho1; mRNA was purified from adult couples of S. mansoni.
                    cDNA was constructed and cloned simultaneously using
                    vector priming with the pBluescript II SK+ vector. cDNA
                    was directionally synthesized from the EcoR1 site in the
                    vector to the Xho1 site."
BASE COUNT       21 a     28 c     27 g     24 t
ORIGIN
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  Query Match             100.0%;  Score 18;  DB 9;  Length 100;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTAAAACGACGGCCAGT 18
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Db      77 TGTAAAACGACGGCCAGT 60
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RESULT  11
AW113079/c
LOCUS       AW113079                100 bp    mRNA    linear   EST 31-JAN-2000
DEFINITION  MC7322 mouse liver, vehicle control Mus musculus cDNA clone MC7322
            3' similar to U43954 Expression vector pBMRz, complete cds, mRNA
            sequence.
ACCESSION   AW113079
VERSION     AW113079.1  GI:6825792
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Thomas,R.S., Rank,D.R., Penn,S.G., Zastrow,G.M., Jovanovich,S. and
            Bradfield,C.A.
  TITLE     McArdle Laboratory/Molecular Dynamics Dioxin EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Bradfield CA
            McArdle Laboratory for Cancer Research
            University of Wisconsin
            1400 University Ave., Madison, WI 53706, USA
            Tel: 608 262 2024
            Fax: 608 262 2824
            Email: bradfield@oncology.wisc.edu
            This clone was sequenced as part of a project to develop a database
            on gene expression changes following exposure to various
            environmental toxicants. The database can be accessed at
            http://mcardle.oncology.wisc.edu/bradfield/. Treatment- dioxane
            vehicle (400 ul/kg). Animals sacrified- 48 hrs post-injection.
            Seq primer: dT(23)V (anchored polyT).
FEATURES            Location/Qualifiers
     source         1. .100
                    /organism="Mus musculus"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="MC7322"
                    /clone_lib="mouse liver, vehicle control"
                    /sex="male"
                    /lab_host="JM109"
                    /note="Organ: liver; Vector: pGEM11Zf (Promega); Site_1:
                    NotI; Site_2: EcoRI; First strand cDNA was primed with a
                    NotI-polyT primer
                    [5'-AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTT-3']
                    Double-stranded cDNA was ligated with EcoRI adapters
                    (Pharmacia), digested with NotI, and ligated into the
                    EcoRI/NotI sites of the pGEM11Zf vector. The library was
                    NOT normalized."
BASE COUNT       24 a     27 c     21 g     27 t      1 others
ORIGIN
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  Query Match             100.0%;  Score 18;  DB 9;  Length 100;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTAAAACGACGGCCAGT 18
           ||||||||||||||||||
Db      49 TGTAAAACGACGGCCAGT 32
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RESULT  12
AW754394
LOCUS       AW754394                100 bp    mRNA    linear   EST 28-APR-2000
DEFINITION  CM0-CT0345-021299-114-f11 CT0345 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW754394
VERSION     AW754394.1  GI:7669326
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM0&t2=CM0-CT0345-
            021299-114-f11&t3=1999-12-02&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 100.
FEATURES            Location/Qualifiers
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     source          1. .100
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="CT0345"
                     /dev_stage="Adult"
                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT       35 a      24 c      29 g      12 t
ORIGIN
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Query Match                 100.0%;  Score 18;  DB 9;  Length 100;
Best Local Similarity   100.0%;  Pred. No. 24;
Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGTAAAACGACGGCCAGT 18
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Db     33 TGTAAAACGACGGCCAGT 50
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RESULT 13
AW812014/c
LOCUS       AW812014                  100 bp    mRNA    linear   EST 17-MAY-2000
DEFINITION  RC6-ST0170-291099-012-B02_1 ST0170 Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   AW812014
VERSION     AW812014.1  GI:7905008
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=RC6-ST0170-291
            099-012-B02_1&t3=1999-10-29&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 100.
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="ST0170"
                     /dev_stage="Adult"
                     /note="Organ: stomach; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       11 a      29 c      24 g      36 t
ORIGIN
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Query Match                 100.0%;  Score 18;  DB 9;  Length 100;
Best Local Similarity   100.0%;  Pred. No. 24;
Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGTAAAACGACGGCCAGT 18
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Db     85 TGTAAAACGACGGCCAGT 68
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RESULT 14
AW812016/c
LOCUS       AW812016                  100 bp    mRNA    linear   EST 17-MAY-2000
DEFINITION  RC6-ST0170-291099-012-D01_1 ST0170 Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   AW812016
VERSION     AW812016.1  GI:7905010
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=RC6-ST0170-291
            099-012-D01_1&t3=1999-10-29&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 86.
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     source          1. .100
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="ST0170"
                     /dev_stage="Adult"
                     /note="Organ: stomach; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       12 a      29 c      23 g      36 t
ORIGIN
```

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Query Match                 100.0%;  Score 18;  DB 9;  Length 100;
Best Local Similarity   100.0%;  Pred. No. 24;
Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 TGTAAAACGACGGCCAGT 18
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Db     68 TGTAAAACGACGGCCAGT 51


RESULT  15
BF901653
LOCUS       BF901653                 100 bp    mRNA    linear   EST 18-JAN-2001
DEFINITION  RC4-MT0161-091200-011-h01 MT0161 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF901653
VERSION     BF901653.1  GI:12293112
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC4&t2=RC4-MT0161-
            091200-011-h01&t3=2000-12-09&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 100.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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                     /clone_lib="MT0161"
                     /dev_stage="Adult"
                     /note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT       38 a     17 c     33 g     12 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db     67 TGTAAAACGACGGCCAGT 84


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Job time: 6478 sec
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